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Sequence Listing was accepted.

See attached Validation Report.

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217-9197 (toll free).

Reviewer: Keisha Douglas

Timestamp: [year=2008; month=9; day=10; hr=12; min=41; sec=21; ms=61;]

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Application No: 10587756 Version No: 2.0

Input Set:

Output Set:

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Started:      2008-08-07 19:48:31.656
Finished:    2008-08-07 19:48:35.857
Elapsed:     0 hr(s) 0 min(s) 4 sec(s) 201 ms
Total Warnings: 3
Total Errors: 36
No. of SeqIDs Defined: 46
Actual SeqID Count: 46

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[illegible]

Input Set:

Output Set:

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Error code	Error Description
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Miyake, Masato
Yoshikawa, Tomohiro
Mikyake, Jun

<120> EVENT SEQUENCES

<130> 690121.409USPC

<140> 10587756

<141> 2008-08-07

<150> PCT/JP2005/001151

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<150> JP 2004-24923

<151> 2004-01-30

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 $\langle 220 \rangle$

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ctg ggg aca gcg gtg ccc tcc acg gga gcc tcg aag agc aag agg cag 96
Leu Gly Thr Ala Val Pro Ser Thr Gly Ala Ser Lys Ser Lys Arg Gln
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gct cag caa atg gtt cag ccc cag tcc ccg gtg gct gtc agt caa agc 144
Ala Gln Gln Met Val Gln Pro Gln Ser Pro Val Ala Val Ser Gln Ser
35 40 45

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 Trp Glu Arg Thr Tyr Leu Gly Asn Ala Leu Val Cys Thr Cys Tyr Gly
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gga agc cga ggt ttt aac tgc gag agt aaa cct gaa gct gaa gag act 288

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gag	cgt	cct	aaa	gac	tcc	atg	atc	tgg	gac	tgt	acc	tgc	atc	ggg	gct	384	
Glu	Arg	Pro	Lys	Asp	Ser	Met	Ile	Trp	Asp	Cys	Thr	Cys	Ile	Gly	Ala		
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Tyr	Gly	His	Cys	Val	Thr	Asp	Ser	Gly	Val	Val	Tyr	Ser	Val	Gly	Met		

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Gly Asn Gly Val Ser Cys Gln Glu Thr Ala Val Thr Gln Thr Tyr Gly				
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Arg Thr Asp Ser Thr Thr Ser Asn Tyr Glu Gln Asp Gln Lys Tyr Ser				
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Ser Gln Leu Arg Asp Gln Cys Ile Val Asp Asp Ile Thr Tyr Asn Val				
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Thr Cys Phe Gly Gln Gly Arg Gly Arg Trp Lys Cys Asp Pro Val Asp				
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Phe Cys Thr Asp His Thr Val Leu Val Gln Thr Arg Gly Gly Asn Ser
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Ile Gly Asp Gln Trp Asp Lys Gln His Asp Met Gly His Met Met Arg
465 470 475 480

Cys Thr Cys Val Gly Asn Gly Arg Gly Glu Trp Thr Cys Ile Ala Tyr
485 490 495

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515 520 525

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530

535

540

Gln Cys Gln Asp Ser Glu Thr Gly Thr Phe Tyr Gln Ile Gly Asp Ser
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Ser Ser Gly Pro Val Glu Val Phe Ile Thr Glu Thr Pro Ser Gln Pro
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Asn Ser His Pro Ile Gln Trp Asn Ala Pro Gln Pro Ser His Ile Ser
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 Ser Leu Ala Asp Gln Glu Ser Cys Lys Gly Arg Cys Thr Gln Gly Phe
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 Met Ala Ser Lys Lys Cys Gln Cys Asp Glu Leu Cys Thr Tyr Tyr Gln
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 Ser Cys Cys Ala Asp Tyr Met Glu Gln Cys Lys Pro Gln Val Thr Arg

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Val Glu Glu Pro Lys Asn Asn Thr Asn Thr Gly Val Gln Pro Glu Asn			
	85	90	95
acc tct cca ccc ggt gac cta aat cct cgg acg gac ggc act cta aag			336
Thr Ser Pro Pro Gly Asp Leu Asn Pro Arg Thr Asp Gly Thr Leu Lys			
	100	105	110
ccg aca gcc ttc cta gat cct gag gaa cag cca agc acc cca gcg cct			384
Pro Thr Ala Phe Leu Asp Pro Glu Glu Gln Pro Ser Thr Pro Ala Pro			
	115	120	125
aaa gtg gag caa cag gag gag atc cta agg ccc gac acc act gat caa			432
Lys Val Glu Gln Gln Glu Glu Ile Leu Arg Pro Asp Thr Thr Asp Gln			
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Ala Leu Leu Gln Arg Asp Ser Trp Glu Asn Ile Phe Glu Leu Leu Phe	
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